APPENDIX A

```
axmi008   ---------GVRGPSHRLS-------NAACVVYGNSRVNVYGWTHTSLKRENIIEANQIT 515
cry1Ca    NS-----VPPREGYSHRLCHATFVQRSGT---PFLTTGVVFSWTHRSATLTNTIDPERIN 468
cry1Aa    NS-----VPPRAGFSHRLSHVTMLSQAAG--AVYTLRAPTFSWQHRSAEFNNIIPSSQIT 471
cry1Ac    NN-----VPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSIT 472
cry1Ia    TG-----QPNYESYSHRLSHIGLISASHVK-ALVYS-----LWTHRSADRTNTIEPNSIT 508
cry2Aa    DLTR----PLHYNQIRNIESPSGTPGGARAYLVSVHNRKNNIYAANENGTMIHLAPEDYT 492
cry3Aa1   TD-----EPLEKGYSHQLNYVMCFLMQGSR-----GTIPVLTWTHKSVDFFNMIDSKKIT 518
cry3Bb    TD-----EPLEKAYSHQLNYAECFLMQDRR-----GTIPFFTWTHRSVDFFNTIDAEKIT 513
cry4Aa    NQGNPTLFPTYDNYSHILSFIKSLSIPATYKTQV----YTFAWTHSSVDPKNTIYHLTT 539
cry4Ba    NQ------PTVNDYTHILSYIKTDVI--DYNSNR----VSFAWTHKIVDPNNQIYTDAIT 481
cry6Aa    SN--------------------------------QYMISHEYTSLPNNFMLSRNS 445
cry7Aa    E-------PIHEKYTHRLCHATAIFKSTP--DYDNATIPIFSWTHRSAEYYNRIYPNKIT 498
cry8Aa    T------VPVAESYSHRLSHITSHSFSKNG-SAYYGSFPVFVWTHTSADLNNTIYSDKIT 527
cry10Aa   EE----------YGHTLSYIKTDNYIFSVVRERRR--VAFSWTHTSVDFQNTIDLDNIT 511
cry16Aa   AK--------YNDYNHILSYMLINGETFGQKRHG----YSFAFTHSSVDPNNTIAANKIT 513
cry19Ba   TT--------YNDYNHILSYMLINGETFGQKRHG----YSFAFTHSSVDRYNTIVPDKIV 507
cry24Aa   G-------NANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDRNNTILPDEIT 516
cry25Aa   HW-----------ISDMMTINQSVQLASNPTQTFAFSALSLGWHHSSAGNRNVYVYDKIT 525
cry39Aa1  LT-------YENYSHILSYMTS-AQHFGDKKIG----YTFAWMHESVDFDNRVDPDKIT 502
cry40Aa1  P--------SYRDYSHRLS-------NAACVGAGNSRINVYGWTHTSMSKYNLIYPDKIT 513
```

```
axmi008   --QIPAVKSYYLQNYLANAYTYVIKGT-HTGGDLIRFLRTKSEYNAVYAGGGIRLIINNK 572
cry1Ca    --QIPLVKGFRVWG------GTSVITGPGFTGGDILRRNTFG---DFVSLQVNINSPI--- 515
cry1Aa    --QIPLTKSTNLGS-----GTSVVKGPGFTGGDILRRTSPG---QISTLRVNITAPL--- 518
cry1Ac    --QIPAVKGNFLFN-----G-SVISGPGFTGGDLVRLNSSG---NNIQNRGYIEVPIHFP 521
cry1Ia    --QIPLVKAFNLSS-----GAAVVRGPGFTGGDILRRTNTG---TFGDIRVNINPPF--- 555
cry2Aa    GFTISPIHATQVNN----QTRTFISEKFGNQGDSLRFEQSN-----------TTARYTLR 537
cry3Aa1   --QLPLVKAYKLQS-----GASVVAGPRFTGGDIIQCTENG---SAATIYVTP-DVSYS- 566
cry3Bb    --QLPVVKAYALSS-----GASIIEGPGFTGGNLLFLKESSN--SIAKFKVTLNSAALL- 563
cry4Aa    --QIPAVKANSLGT-----ASKVVQGPGHTGGDLIDFKDH---------FKITCQHSNF- 582
cry4Ba    --QVPAVKSNFLNA-----TAKVIKGPGHTGGDLVALTSNGT--LSGR-MEIQCKTSIFN 531
cry6Aa    ----------------------------------------------------------
cry7Aa    --KIPAVKMYKLDD-----PSTVVKGPGFTGGDLVKRGSTG---YIGDIKATVNSPL--- 545
cry8Aa    --QIPAVKGDMLYL-----GGSVVQGPGFTGGDILKRTNPS---ILGTFAVTVNGSL--- 574
cry10Aa   --QIHALKALKVSS-----DSKIVKGPGHTGGDLVILKDS----------MDFRVRFLK 553
cry16Aa   --QIPVVKASSING-----SISIEKGPGFTGGDLVKMRADS---------GLTMRFKAE 556
cry19Ba   --QIPAVKTNLVG-------ANIIKGPGHTGGDLIKLEYER---------FLSLRIK-L 547
cry24Aa   --QIPAVTAYELR-----GNSSVVAGPGSTGGDLVKMS----------YHSVWSFKVYC 558
cry25Aa   --QIPATKTVREHP--------MIKGPGFTGGDLADLSSNSD----ILQYDLRSDYDDRL 571
cry39Aa1  --QIPAVKGDYLQY------GYVKQGPGHTGGDLVSMIRTD----------RLGINVY-F 543
cry40Aa1  --QIPAVKAFDIS---DTGPGQVIAGPGHTGGNVVSLP--------YYSRLKIRLIP--A 558
```

HIGHLIGHTED SEQUENCES = Blocks A-F (de Maagd *et al.* (1999) *Appl. Environ. Microbiol.* 65:4369-4374)

BLOCKED SEQUENCES = Conserved domains 3-5

```
axmi008    TAGQSYRIRFRYAADKAAFFSVYLYPGGWGSN------RFVSLEKSYSGNYDDLKYSDFK  626
cry1Ca     --TQRYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGE---NLTSRTFR  570
cry1Aa     --SQRYRVRIRYASTTNLQFHTSIDGRPINQG-------NFSATMSSGS---NLQSGSFR  566
cry1Ac     STSTRYRVRVRYASVTPIHLNVNWGNSSIFSN-------TVPATATSLD---NLQSSDFG  571
cry1Ia     --AQRYRVRIRYASTTDLQFHTSINGKAINQG-------NFSATMNRGE---DLDYKTFR  603
cry2Aa     GNGNSYNLYLRVSSIGNSTIRVTINGRVYTVS-------NVNTTTNNDG----VNDNGAR  586
cry3Aa1    ---QKYRARIHYASTSQITFTLSLDGAPFNQY-------YFDKTINKGD---TLTYNSFN  613
cry3Bb     ---QRYRVRIRYASTTNLRLFVQNSNNDFLVI-------YINKTMNKDD---DLTYQTFD  610
cry4Aa     --QQSYFIRIRYASNGSANTRAVINLSIPGVAELG-MALNPTFSGTD---YTNLKYKDFQ  636
cry4Ba     DPTRSYGLRIRYAAN--SPIVLNVSYVLQGVSRGTTISTESTFSRPNNIIPTDLKYEEFR  589
cry6Aa     ---I-----NLEYKQPENNFMIYWYNNSDWYNN--------------------------  469
cry7Aa     --SQKYRVRVRYATNVSGQFNVYINDKITLQT----KFQNTVETIGEGK---DLTYGSFG  596
cry8Aa     --SQRYRVRIRYASTTDFEFTLYLG-DTIEKN-------RFNKTMDNGA---SLTYETFK  621
cry10Aa    NVSRQYQVRIRYATNAPKTTVFLTGIDTISVELPSTTSRQNPN-------ATDLTYADFG  606
cry16Aa    LLDKKYRVRIRYKQNYSSKLILRKWKGEGYIQQQIHNIS--PTYGAFSY---------LE  605
cry19Ba    IASMTFRIRIRYASNISGQMMINIGYQNPTYFNIIPTTS--RDYTELK---------FE  595
cry24Aa    SELKNYRVRIRYASHGNCQFLMKRWPSTGVAP------RQWARHNVQGTFSNSMRYEAFK  612
cry25Aa    TEDVPFRIRIRCASIGVSTISVDNWGSSSPQVT------VASTAASLDT----LKYESFQ  621
cry39Aa1   PQPLDYRIRIRYSTSSNGYLYIYSPNTKIVYLPPTTLVDGQPTFDPMD---------FS  593
cry40Aa1   STNKNYLVRVRYTSTSNGRLLVERWSPSSIIN------SYFFLPSTGPG--DSFGYVDTL  610


axmi008    FAEIITPPLPSSNIQMDVEMQANSFQS----DVNVVLDKIEFLPSNTTTLEYEGERDLEK  682
cry1Ca     YTDFSNPFSFRANPDIIGISEQPLFGAGSISSGELYIDKIETILADATFEA---ESDLER  627
cry1Aa     TVGFTTPFNFSNGSSVFTLSAHVFN-----SGNEVYIDRIEFVPAEVTFEA---EYDLER  618
cry1Ac     YFESANAFTSSLGN---IVGVRNFS-----GTAGVIIDRFEFIPVTATLEA---EYNLER  620
cry1Ia     TVGFTTPFSFLDVQSTFTIGAWNFS-----SGNEVYIDRIEFVPVEVTYEA---EYDFEK  655
cry2Aa     FSDINIGNIVASDNTNVTLDINVTLNS----GTPFDLMNIMFVPTNLPPLY--------  633
cry3Aa1    LASFSTPFELSG--NNLQIGVTGLS-----AGDKVYIDKIEFIPVN------------  652
cry3Bb     LATTNSNMGFSGDKNELIIGAESFV-----SNEKIYIDKIEFIPVQL-----------  652
cry4Aa     YLEFSN---EVKFAPNQNISLVFNRSD-VYTNTTVLIDKIEFLPITRSIREDREKQLET  692
cry4Ba     YKDPFDAIVPMRLSSNQLITIAIQPLN-MTSNNQVIIDRIEIIPITQSVLDETENQNLES  648
cry6Aa     -SDWYNN-----------------------------------------  475
cry7Aa     YIEYSTTIQFPDEHPKITLHLSDLS-----NNSSFYVDSIEFIPVDVNYAE---KEKLEK  648
cry8Aa     FASFITDFQFRETQDKILLSMGDFS-----SGQEVYIDRIEFIPVDETYEA---EQDLEA  673
cry10Aa    YVTFPRTVPNKTFEGEDTLLMTLYGTP-NHSYN-IYIDKIEFIPITQSVLDYTEKQNIEK  664
cry16Aa    SFTITTTENIFDLTMEVTYPYGRQFVE-DIPS--LILDKIEFLPTN-----------  648
cry19Ba    DFQLVDTSYIYSGGPSISS--NTLWLD-NFSNGPVIIDKIEFIPLGITLNQAQGYDTYDQ  652
cry24Aa    YLDIFTITP-----EENNFAFTIDLES----GGDLFIDKIEFIPVSGSAFEYEGKQNIEK  663
cry25Aa    YVSIPGNYYFDSAPRIRLLR---------QPGRLLVDRIEIIPVNFFPLS-------EQ  664
cry39Aa1   AFRVVEVPASFR--ASVAG--YTNFTI-EAGFGPVYIDKIEFIPDNTTTLEYEGGRDLEK  648
cry40Aa1   VTTFNQP---------GVEIIIQNLDT----PIN--VDKVEFIPVNSTALEYEGKQSLEK  655
```